



1600

RAW SEQUENCE LISTING

DATE: 09/12/2002

PATENT APPLICATION: US/10/080,980A

TIME: 10:15:41

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF4\09122002\J080980A.raw

3 <110> APPLICANT: Bristol-Myers Squibb Company
 5 <120> TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL
 BETA-SUBUNIT,

6 K+betaM6, EXPRESSED HIGHLY IN THE SMALL INTESTINE

8 <130> FILE REFERENCE: D0121 NP

C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/080,980A

C--> 10 <141> CURRENT FILING DATE: 2002-02-21

10 <150> PRIOR APPLICATION NUMBER: US 60/270,132

11 <151> PRIOR FILING DATE: 2001-02-21

13 <150> PRIOR APPLICATION NUMBER: US 60/278,953

14 <151> PRIOR FILING DATE: 2001-03-27

16 <160> NUMBER OF SEQ ID NOS: 74

18 <170> SOFTWARE: PatentIn version 3.0

20 <210> SEQ ID NO: 1

21 <211> LENGTH: 2052

22 <212> TYPE: DNA

23 <213> ORGANISM: homo sapiens

25 <220> FEATURE:

26 <221> NAME/KEY: CDS

27 <222> LOCATION: (121)..(1095)

29 <400> SEQUENCE: 1

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30 cgtccggcgg ggccagggc tgagcgagcg tccgggctcc ggggctccgg ggaaggcggt      60
32 tgcagctcct gactgcagcg cggcttcctg ccaatgtccc ggccgggcca cctctctgtc      120
34 atg gct ctg gcg gac agc aca cgt gga tta ccc aac ggg ggc ggc ggc      168
35 Met Ala Leu Ala Asp Ser Thr Arg Gly Leu Pro Asn Gly Gly Gly Gly
36 1          5          10          15
38 ggg ggc ggc agt ggc tcc tcg tcg tcc tcc gcg gag cca ccg ctc ttc      216
39 Gly Gly Gly Ser Gly Ser Ser Ser Ser Ser Ala Glu Pro Pro Leu Phe
40          20          25          30
42 ccc gac atc gtg gag ctg aac gtg ggg ggc cag gtg tac gtg acc cgg      264
43 Pro Asp Ile Val Glu Leu Asn Val Gly Gly Gln Val Tyr Val Thr Arg
44          35          40          45
46 cgc tgc acg gtg gtg tcg gtg ccc gac tcg ctg ctc tgg cgc atg ttc      312
47 Arg Cys Thr Val Val Ser Val Pro Asp Ser Leu Leu Trp Arg Met Phe
48          50          55          60
50 acg cag cag cag ccg cag gag ctg gcc cgg gac agc aaa ggc cgc ttc      360
51 Thr Gln Gln Gln Pro Gln Glu Leu Ala Arg Asp Ser Lys Gly Arg Phe
52 65          70          75          80
54 ttt ctg gac cgg gac ggc ttc ctc ttc cgc tac atc ctg gat tac ctg      408
55 Phe Leu Asp Arg Asp Gly Phe Leu Phe Arg Tyr Ile Leu Asp Tyr Leu
56          85          90          95
58 cgg gac ttg cag ctc gtg ctg ccc gac tac ttc ccc gag cgc agc cgg      456
59 Arg Asp Leu Gln Leu Val Leu Pro Asp Tyr Phe Pro Glu Arg Ser Arg
60          100          105          110

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62 ctg cag cgc gag gcc gag tac ttc gag ctg cca gag ctg gtg cgc cgc      504
63 Leu Gln Arg Glu Ala Glu Tyr Phe Glu Leu Pro Glu Leu Val Arg Arg
64      115      120      125
66 ctg ggg ggc ccc cag cag ccc ggc ccg ggg ccg ccg ccc tgg cgg cgc      552
67 Leu Gly Ala Pro Gln Gln Pro Gly Pro Gly Pro Pro Pro Ser Arg Arg
68      130      135      140
70 ggg gtg cac aag gag ggc tgg ctg ggt gac gag ctg ctg ccg ctt ggc      600
71 Gly Val His Lys Glu Gly Ser Leu Gly Asp Glu Leu Leu Pro Leu Gly
72 145      150      155      160
74 tac tgg gag ccc gaa cag cag gag ggc gcc tct gcc ggg ggc ccg tgg      648
75 Tyr Ser Glu Pro Glu Gln Gln Glu Gly Ala Ser Ala Gly Ala Pro Ser
76      165      170      175
78 ccc acg ctg gag ctg gct agc cgc agt ccg tcc ggg gcc ggc gcc gcc      696
79 Pro Thr Leu Glu Leu Ala Ser Arg Ser Pro Ser Gly Gly Ala Ala Gly
80      180      185      190
82 ccg ctg ctg acg ccg tcc cag tgg ctg gac gcc agc ccg cgc tgg gcc      744
83 Pro Leu Leu Thr Pro Ser Gln Ser Leu Asp Gly Ser Arg Arg Ser Gly
84      195      200      205
86 tac atc acc atc gcc tac cgc gcc tcc tac acc atc ggg ccg gac gcc      792
87 Tyr Ile Thr Ile Gly Tyr Arg Gly Ser Tyr Thr Ile Gly Arg Asp Ala
88      210      215      220
90 cag gcc gac gcc aag ttc cgg cga gtg gcc cgc atc acc gtt tgc gga      840
91 Gln Ala Asp Ala Lys Phe Arg Arg Val Ala Arg Ile Thr Val Cys Gly
92 225      230      235      240
94 aag acg tgg ctg gcc aag gag gtg ttt ggg gac acc ctg aac gaa agc      888
95 Lys Thr Ser Leu Ala Lys Glu Val Phe Gly Asp Thr Leu Asn Glu Ser
96      245      250      255
98 cgg gac ccc gac cgt ccc ccg gag cgc tac acc tgg cgc tat tac ctg      936
99 Arg Asp Pro Asp Arg Pro Pro Glu Arg Tyr Thr Ser Arg Tyr Tyr Leu
100      260      265      270
102 aag ttc aac ttc ctg gag cag gcc ttc gac aag ctg tcc gag tgg gcc      984
103 Lys Phe Asn Phe Leu Glu Gln Ala Phe Asp Lys Leu Ser Glu Ser Gly
104      275      280      285
106 ttc cac atg gtg gcc tgc agc tcc acg gcc acc tgc gcc ttt gcc agc      1032
107 Phe His Met Val Ala Cys Ser Ser Thr Gly Thr Cys Ala Phe Ala Ser
108      290      295      300
110 agc acc gac cag agc gag gac aag atc tgg acc agc tac acc gag tac      1080
111 Ser Thr Asp Gln Ser Glu Asp Lys Ile Trp Thr Ser Tyr Thr Glu Tyr
112 305      310      315      320
114 gtc ttc tgc agg gag tgagctcccc agacccccctc gccactccag cgcgccgtcc      1135
115 Val Phe Cys Arg Glu
116      325
118 ttctctgtgc cgagagatga ttacagagcc tcttggtcca cctttgtccc ctggctgctg      1195
120 cctccatt ctccccctcc agtagtagct gggtagagcc tgtccgcca ccttccctcc      1255
122 actacagaac ctgcagccgc aaatcctctg ggcgtcttgg tcttctttgg acctcctgaa      1315
124 ccgagagaac ccagaggaac cccaccccca ccccaacctc ccaactccatg cttctcttac      1375
126 tccctgcttc aaaccacccc tccccagat ggtacttcag ttgggatcta ttgggggagt      1435
128 gtggccacag accgggggat gattgaattg ttcagaacct gattggacgg tgtccaatgt      1495
130 ggggaagatt tcttgaaat cttctcaagc tcttatgact cactgggggt ttaagagatc      1555

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132 aggattgggt ccactgtctg gggttagtgt tttacaaggt cattacacag tctttttgac 1615
134 ctcttttgaa ggtagagttt tagaaggctg gatggaagat tctgagcctg gaattaggac 1675
136 cccatggagg cagtcctcaa accaccctc cccagatgg tacttcagtt tggatctatt 1735
138 gggggagtggt ggccacagac cgggggatga ttgaattgtt cagaacctga ttggaccgtg 1795
140 tccaatgtgc ggaagatttc ctgaaaatct tctcaagctc ttatgactca ctgggggttt 1855
142 aagagatcag gattggttcc actgtctggg gttagtgttt tacaaggctc ttacacagtc 1915
144 tttttgacct cttttgaagg tagagtttta gaaggctgga tggaagattc tgagcctgga 1975
146 attaggaccc catggaggca gttcagtaac taaactaata aagttttgaa aagttacacg 2035
148 taaaaaaaaa aaaaaaa
151 <210> SEQ ID NO: 2
152 <211> LENGTH: 325
153 <212> TYPE: PRT
154 <213> ORGANISM: homo sapiens
156 <400> SEQUENCE: 2
158 Met Ala Leu Ala Asp Ser Thr Arg Gly Leu Pro Asn Gly Gly Gly Gly
159 1 5 10 15
162 Gly Gly Gly Ser Gly Ser Ser Ser Ser Ser Ala Glu Pro Pro Leu Phe
163 20 25 30
166 Pro Asp Ile Val Glu Leu Asn Val Gly Gly Gln Val Val Thr Arg
167 35 40 45
170 Arg Cys Thr Val Val Ser Val Pro Asp Ser Leu Leu Trp Arg Met Phe
171 50 55 60
174 Thr Gln Gln Gln Pro Gln Glu Leu Ala Arg Asp Ser Lys Gly Arg Phe
175 65 70 75 80
178 Phe Leu Asp Arg Asp Gly Phe Leu Phe Arg Tyr Ile Leu Asp Tyr Leu
179 85 90 95
182 Arg Asp Leu Gln Leu Val Leu Pro Asp Tyr Phe Pro Glu Arg Ser Arg
183 100 105 110
186 Leu Gln Arg Glu Ala Glu Tyr Phe Glu Leu Pro Glu Leu Val Arg Arg
187 115 120 125
190 Leu Gly Ala Pro Gln Gln Pro Gly Pro Gly Pro Pro Pro Ser Arg Arg
191 130 135 140
194 Gly Val His Lys Glu Gly Ser Leu Gly Asp Glu Leu Leu Pro Leu Gly
195 145 150 155 160
198 Tyr Ser Glu Pro Glu Gln Gln Glu Gly Ala Ser Ala Gly Ala Pro Ser
199 165 170 175
202 Pro Thr Leu Glu Leu Ala Ser Arg Ser Pro Ser Gly Gly Ala Ala Gly
203 180 185 190
206 Pro Leu Leu Thr Pro Ser Gln Ser Leu Asp Gly Ser Arg Arg Ser Gly
207 195 200 205
210 Tyr Ile Thr Ile Gly Tyr Arg Gly Ser Tyr Thr Ile Gly Arg Asp Ala
211 210 215 220
214 Gln Ala Asp Ala Lys Phe Arg Arg Val Ala Arg Ile Thr Val Cys Gly
215 225 230 235 240
218 Lys Thr Ser Leu Ala Lys Glu Val Phe Gly Asp Thr Leu Asn Glu Ser
219 245 250 255
222 Arg Asp Pro Asp Arg Pro Pro Glu Arg Tyr Thr Ser Arg Tyr Tyr Leu
223 260 265 270
226 Lys Phe Asn Phe Leu Glu Gln Ala Phe Asp Lys Leu Ser Glu Ser Gly

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227           275           280           285
230 Phe His Met Val Ala Cys Ser Ser Thr Gly Thr Cys Ala Phe Ala Ser
231           290           295           300
234 Ser Thr Asp Gln Ser Glu Asp Lys Ile Trp Thr Ser Tyr Thr Glu Tyr
235 305           310           315           320
238 Val Phe Cys Arg Glu
239           325
242 <210> SEQ ID NO: 3
243 <211> LENGTH: 228
244 <212> TYPE: PRT
245 <213> ORGANISM: Drosophila melanogaster
247 <400> SEQUENCE: 3
249 Met Pro Glu Ile Ile Glu Leu Asn Val Gly Gly Val Ser Tyr Thr Thr
250 1           5           10           15
252 Thr Leu Ala Thr Leu Leu Gln Asp Lys Ser Thr Leu Leu Ala Glu Leu
253           20           25           30
255 Phe Gly Glu Gly Arg Asp Ser Leu Ala Lys Asp Ser Lys Gly Arg Tyr
256           35           40           45
258 Phe Leu Asp Arg Asp Gly Val Leu Phe Arg Tyr Ile Leu Asp Phe Leu
259           50           55           60
261 Arg Asp Lys Ala Leu His Leu Pro Glu Gly Phe Arg Glu Arg Gln Arg
262 65           70           75           80
264 Leu Leu Arg Glu Ala Glu His Phe Lys Leu Thr Ala Met Leu Glu Cys
265           85           90           95
267 Ile Arg Ser Glu Arg Asp Ala Arg Pro Pro Gly Cys Ile Thr Ile Gly
268           100          105          110
270 Tyr Arg Gly Ser Phe Gln Phe Gly Lys Asp Gly Leu Ala Asp Val Lys
271           115          120          125
273 Phe Arg Lys Leu Ser Arg Ile Leu Val Cys Gly Arg Val Ala Gln Cys
274           130          135          140
276 Arg Glu Val Phe Gly Asp Thr Leu Asn Glu Ser Arg Asp Pro Asp His
277 145          150          155          160
279 Gly Gly Thr Asp Arg Tyr Thr Ser Arg Phe Phe Leu Lys His Cys Tyr
280           165          170          175
282 Ile Glu Gln Ala Phe Asp Asn Leu His Asp His Gly Tyr Arg Met Ala
283           180          185          190
285 Gly Ser Cys Gly Ser Gly Thr Ala Gly Ser Ala Ala Glu Pro Lys Pro
286           195          200          205
288 Gly Val Asp Thr Glu Glu Asn Arg Trp Asn His Tyr Asn Glu Phe Val
289           210          215          220
291 Phe Ile Arg Asp
292 225
294 <210> SEQ ID NO: 4
295 <211> LENGTH: 435
296 <212> TYPE: PRT
297 <213> ORGANISM: Homo sapiens
299 <400> SEQUENCE: 4
301 Gln Gln Gln Lys Lys Gly Thr Met Ala Leu Ser Gly Asn Cys Ser Arg
302 1           5           10           15

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304 Tyr Tyr Pro Arg Glu Gln Gly Ser Ala Val Pro Asn Ser Phe Pro Glu
305          20          25          30
307 Val Val Glu Leu Asn Val Gly Gly Gln Val Tyr Phe Thr Arg His Ser
308          35          40          45
310 Thr Leu Ile Ser Ile Pro His Ser Leu Leu Trp Lys Met Phe Ser Pro
311          50          55          60
313 Lys Arg Asp Thr Ala Asn Asp Leu Ala Lys Asp Ser Lys Gly Arg Phe
314 65          70          75          80
316 Phe Ile Asp Arg Asp Gly Phe Leu Phe Arg Tyr Ile Leu Asp Tyr Leu
317          85          90          95
319 Arg Asp Arg Gln Val Val Leu Pro Asp His Phe Pro Glu Lys Gly Arg
320          100          105          110
322 Leu Lys Arg Glu Ala Glu Tyr Phe Gln Leu Pro Asp Leu Val Lys Leu
323          115          120          125
325 Leu Thr Pro Asp Glu Ile Lys Gln Ser Pro Asp Glu Phe Cys His Ser
326          130          135          140
328 Asp Phe Glu Asp Ala Ser Gln Gly Ser Asp Thr Arg Ile Cys Pro Pro
329 145          150          155          160
331 Ser Ser Leu Leu Pro Ala Asp Arg Lys Trp Gly Phe Ile Thr Val Gly
332          165          170          175
334 Tyr Arg Gly Ser Cys Thr Leu Gly Arg Glu Gly Gln Ala Asp Ala Lys
335          180          185          190
337 Phe Arg Arg Val Pro Arg Ile Leu Val Cys Gly Arg Ile Ser Leu Ala
338          195          200          205
340 Lys Glu Val Phe Gly Glu Thr Leu Asn Glu Ser Arg Asp Pro Asp Arg
341          210          215          220
343 Ala Pro Glu Arg Tyr Thr Ser Arg Phe Tyr Leu Lys Phe Lys His Leu
344 225          230          235          240
346 Glu Arg Ala Phe Asp Met Leu Ser Glu Cys Gly Phe His Met Val Ala
347          245          250          255
349 Cys Asn Ser Ser Val Thr Ala Ser Phe Ile Asn Gln Tyr Thr Asp Asp
350          260          265          270
352 Lys Ile Trp Ser Ser Tyr Thr Glu Tyr Val Phe Tyr Arg Glu Pro Ser
353          275          280          285
355 Arg Trp Ser Pro Ser His Cys Asp Cys Cys Cys Lys Asn Gly Lys Gly
356          290          295          300
358 Asp Lys Glu Gly Glu Ser Gly Thr Ser Cys Asn Asp Leu Ser Thr Ser
359 305          310          315          320
361 Ser Cys Asp Ser Gln Ser Glu Ala Ser Ser Pro Gln Glu Thr Val Ile
362          325          330          335
364 Cys Gly Pro Val Thr Arg Gln Thr Asn Ile Gln Thr Leu Asp Arg Pro
365          340          345          350
367 Ile Lys Lys Gly Pro Val Gln Leu Ile Gln Gln Ser Glu Met Arg Arg
368          355          360          365
370 Lys Ser Asp Leu Leu Arg Thr Leu Thr Ser Gly Ser Arg Glu Ser Asn
371          370          375          380
373 Met Ser Ser Lys Lys Lys Ala Val Lys Glu Lys Leu Ser Ile Glu Glu
374 385          390          395          400
376 Glu Leu Glu Lys Cys Ile Gln Asp Phe Leu Lys Ile Lys Ile Pro Asp

```

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/080,980A

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:6; Xaa Pos. 15
Seq#:8; N Pos. 146,147,148,149,150,151,152,153,154,155,156,157,158,159,160
Seq#:8; N Pos. 161,162,163,164,165,166,167,488,489,490,491,492,493,494,495
Seq#:8; N Pos. 496,497,498,499,500,501,502,503,504,505,506,507,508,509,510
Seq#:8; N Pos. 511,512,513,514,515,516,517,518,519,520,521,522,523,524,525
Seq#:8; N Pos. 526,527,528,529,530,531,532,533,534,535,536,537,538,539,540
Seq#:8; N Pos. 541,542,543,544,545,546,670,671,672,673,674,675,676,677,678
Seq#:8; N Pos. 679,680,681,682,683,684,685,686,687,688

VARIABLE LOCATION SUMMARY
PATENT APPLICATION: US/10/080,980A

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Use of n's or Xaa's(NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:6; Xaa Pos. 15
Seq#:8; N Pos. 146,147,148,149,150,151,152,153,154,155,156,157,158,159,160
Seq#:8; N Pos. 161,162,163,164,165,166,167,488,489,490,491,492,493,494,495
Seq#:8; N Pos. 496,497,498,499,500,501,502,503,504,505,506,507,508,509,510
Seq#:8; N Pos. 511,512,513,514,515,516,517,518,519,520,521,522,523,524,525
Seq#:8; N Pos. 526,527,528,529,530,531,532,533,534,535,536,537,538,539,540
Seq#:8; N Pos. 541,542,543,544,545,546,670,671,672,673,674,675,676,677,678
Seq#:8; N Pos. 679,680,681,682,683,684,685,686,687,688

VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:432 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:547 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:547 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:120
L:559 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:559 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:480
L:561 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:561 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:540
L:565 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:565 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:660